



OIPE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/817,774

DATE: 01/19/2002
 TIME: 11:18:44

Input Set : A:\seqlist.txt
 Output Set: N:\CRF3\01192002\I817774.raw

3 <110> APPLICANT: CHOE, Sunghwa
 4 FELDMANN A., Kenneth
 6 <120> TITLE OF INVENTION: Dwf5 MUTANTS
 8 <130> FILE REFERENCE: 2225-0020 / 91020.002
 10 <140> CURRENT APPLICATION NUMBER: 09/817,774
 11 <141> CURRENT FILING DATE: 2001-03-26
 13 <150> PRIOR APPLICATION NUMBER: 60/192,202
 14 <151> PRIOR FILING DATE: 2000-03-27
 16 <160> NUMBER OF SEQ ID NOS: 45
 18 <170> SOFTWARE: PatentIn Ver. 2.0

**Does Not Comply
 Corrected Diskette Needed**

ERRORED SEQUENCES

2416 <210> SEQ ID NO: 36
 2417 <211> LENGTH: 4880
 2418 <212> TYPE: DNA
 2419 <213> ORGANISM: Arabidopsis thaliana
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 2438 <222> LOCATION: (1505)..(1606)
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 2443 <222> LOCATION: (1711)..(1776)
 2444 <223> OTHER INFORMATION: dwf5-3
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 2447 <221> NAME/KEY: CDS
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 2449 <223> OTHER INFORMATION: dwf5-3
 2451 <220> FEATURE:

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2468 <222> LOCATION: (3494)..(3559)
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2486 attgcatctc ttaaacatac taaaatttct ggaaatgaaa aaaaactgag aaacgcaaaa 180
2488 gaattcaaca cagcatcaga aaactagatc taggtttcgc cgggagttac caaaaacatt 240
2490 agaaaaaatc gatacttaca cgaattcaac caattctgga gaattttctt ccaaggcaag 300
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2494 tttgattttg ttagtctcga ttcatcacta tgtgttgaat acagagatga cgaagatctt 420
2496 ttgaggggtg agagagaaga agctaagaag attgggatca atcaaaaacg atggcgaga 480
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2502 actctgttga ttagtcaaca cagatcagaa tctgaggctt tggccgagac gagagaagca 660
2504 gaagaagaaa atg gcg gag act gta cat tct ccg atc gtt act tac gca 709
2505 Met Ala Glu Thr Val His Ser Pro Ile Val Thr Tyr Ala
2506 1 5 10
2508 tcg atg tta tcg ctt ctc gcc ttc tgt cca cct ttc gtc att ctc ctg 757
2509 Ser Met Leu Ser Leu Leu Ala Phe Cys Pro Pro Phe Val Ile Leu Leu
2510 15 20 25
2512 taagctcatc aatttctgat tcgcaagtct ttattctagt tctcagatca gactcgcaca 817
2514 cttttctggc tccttaattc atagcgagaa gtgcatagcc gatattctta aatcctttcc 877
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2518 ggccaatgtg agtttccaga tttttaggaa acaagggtag atttaaagct acaaaatcat 997
2520 atttagtgag ttttaagtaa tgctcacaag tttcatttct ttatgatgca ga tgg tac 1055
2521 Trp Tyr
2522 30
2524 aca atg gtt cat cag gat ggt tct gtt act cag acc ttt ggc ttc ttt 1103

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2529 Trp Glu Asn Gly Val Gln Gly Leu Ile Asn Ile Trp Pro Arg Pro Thr
2530          50                      55                      60
2532 ttg att gct tgg aaa att ata ttt tgc tat gga gca ttt gaa gct att 1199
2533 Leu Ile Ala Trp Lys Ile Ile Phe Cys Tyr Gly Ala Phe Glu Ala Ile
2534          65                      70                      75
2536 ctt cag ctg ctt ctg cct ggt aaa aga gtt gag ggt cca ata tct cca 1247
2537 Leu Gln Leu Leu Leu Pro Gly Lys Arg Val Glu Gly Pro Ile Ser Pro
2538          80                      85                      90                      95
2540 gcc gga aac cga cca gtt tac aag gtatgttcaa ttagtcttgt gtggtggaag 1301
2541 Ala Gly Asn Arg Pro Val Tyr Lys
2542          100
2544 ttgatgcaga tgacaactgt acggttcttt tcttgcag gcc aat ggt ctg gct gct 1357
2545                      Ala Asn Gly Leu Ala Ala
2546                      105
2548 tac ttt gtg aca cta gca acc tat ctt ggt ctt tgg tgg taagaaatgt 1406
2549 Tyr Phe Val Thr Leu Ala Thr Tyr Leu Gly Leu Trp Trp
2550          110                      115                      120
2552 ttccgatgac ttggttttg tttaagttat tgtttacgta tcttaagctt ggattaagtg 1466
2554 ttgcacctat gtgagttaat ttctgtgcgt tattcagg ttt gga atc ttc aac cct 1522
2555                      Phe Gly Ile Phe Asn Pro
2556                      125
2558 gca att gtc tat gat cac ttg ggt gaa ata ttt tcg gca cta ata ttc 1570
2559 Ala Ile Val Tyr Asp His Leu Gly Glu Ile Phe Ser Ala Leu Ile Phe
2560          130                      135                      140
2562 gga agc ttc ata ttt tgt gtt ttg ttg tac ata aaa gtaagtgtct 1616
2563 Gly Ser Phe Ile Phe Cys Val Leu Leu Tyr Ile Lys
2564          145                      150                      155
2566 attgcatgaa tgggtgtgtt ttgttttct tagtctctat tttttagaaa ttgaccttt 1676
2568 tgtgttgcta aaacttattt ttttcttgt acag ggc cat gtt gca cct tca tca 1731
2569                      Gly His Val Ala Pro Ser Ser
2570                      160
2572 agt gac tct ggt tca tgt ggt aac cta ata att gac ttc tat tgg 1776
2573 Ser Asp Ser Gly Ser Cys Gly Asn Leu Ile Ile Asp Phe Tyr Trp
2574          165                      170                      175
2576 gtgagttatt tctgctgac agatctcatt ctttttgaaa ttgcttggtg ggatttattt 1836
2578 gaggaactct ggtcttacta gccatctcct cataatattt ttgcctcttt tctcgacatt 1896
2580 tggaggtcaa gtttactaa agtttccaat ttagtagac ctgtaaacgg aaatgttctt 1956
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2584 tcggtgaagg aaaagaacaa agtatgcagt agttattata acaatatcaa gttgagatct 2076
2586 tctctcacca tgtactcttt tgcctcaact tatcattaac acaatccaat ttgtggcaat 2136
2588 cttttctcac tgtgtttttt cgcgtcgtgc tttgcag ggc atg gag ttg tac cct 2191
2589                      Gly Met Glu Leu Tyr Pro
2590                      180
2592 cga att ggt aag agc ttt gac atc aag gtg ttt act aat tgc aga ttc 2239
2593 Arg Ile Gly Lys Ser Phe Asp Ile Lys Val Phe Thr Asn Cys Arg Phe
2594          185                      190                      195                      200

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2596 gga atg atg tct tgg gca gtt ctt gca gtc acg tac tgc ata aaa cag      2287
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2600 gtattttctg gataattctt atgtaaatac tacactctga cgacatagtc tgggtggtttc 2347
2602 tttaagtctt tatttcatta gagagcttca cctctttctg atttgtgatt cctgtacttt 2407
2604 ctttaaccag tat gaa ata aat ggc aaa gta tct gat tca atg ctg gtg      2456
2605                Tyr Glu Ile Asn Gly Lys Val Ser Asp Ser Met Leu Val
2606                220                225
2608 aac acc atc ctg atg ctg gtg tat gtc aca aaa ttc ttc tgg tgg gaa      2504
2609 Asn Thr Ile Leu Met Leu Val Tyr Val Thr Lys Phe Phe Trp Trp Glu
2610 230                235                240                245
2612 gct ggt tat tgg aac acc atg gac att gca cat gac cga ggt      2546
2613 Ala Gly Tyr Trp Asn Thr Met Asp Ile Ala His Asp Arg Gly
2614                250                255
2616 atgcttctgg tacatatata aaatttatat catcacatcc tcatataggg tacaaggaaa 2606
2618 gaaagccagt agtaataaca aaagtttctc tactgtttgg ctataatttc cttgccagtt 2666
2620 ctgtttatat ggctaaggca gcagcatatt attcagatta ttgttactgg ctttaacaca 2726
2622 tgaacttaag cttacttttc aatgctttat aatttatgat tcttcagct gga ttc tat 2784
2623                Gly Phe Tyr
2624                260
2626 ata tgc tgg ggt tgt cta gtg tgg gtg cct tct gtc tac act tct cca      2832
2627 Ile Cys Trp Gly Cys Leu Val Trp Val Pro Ser Val Tyr Thr Ser Pro
2628                265                270                275
2630 ggc atg tac ctt gtg aac cac ccc gtc gaa ctc gga act cag      2874
2631 Gly Met Tyr Leu Val Asn His Pro Val Glu Leu Gly Thr Gln
2632                280                285                290
2634 gtgcataatt ttgaatttgt ctagaagaaa gaaatcgtct ttgtgtgtta atccaatgag 2934
2636 aaacttttag gataccactt ttttatacga aaaaaaacia gtaagggttg gctaaatgtg 2994
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2648                295                300
2650 att ctg tgc att tac ata aac tat gac tgt gat aga caa agg caa gag      3333
2651 Ile Leu Cys Ile Tyr Ile Asn Tyr Asp Cys Asp Arg Gln Arg Gln Glu
2652                305                310                315
2654 ttc agg agg aca aac ggg aaa tgt ttg gtt tgg gga aga gcc ccg tca      3381
2655 Phe Arg Arg Thr Asn Gly Lys Cys Leu Val Trp Gly Arg Ala Pro Ser
2656                320                325                330
2658 aag gtgtgatcat aataagcccc aactagctta gtgaacttag ctatattcct      3434
2659 Lys
2661 tttcagacct aaacattttg atgtgtatga atctctcttg gtctctcggg ttgttgca 3493
2663 att gtg gcg tog tat act aca aca tct ggt gaa act aaa act agt ctt      3541
2664 Ile Val Ala Ser Tyr Thr Thr Thr Ser Gly Glu Thr Lys Thr Ser Leu
2665 335                340                345                350
2667 ctc tta acg tct gga tgg tgagactatt ctacattata cagttacaac      3589
2668 Leu Leu Thr Ser Gly Trp

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2675 Ala Arg His Phe His Tyr Val Pro Glu Ile Leu Ser Ala Phe Phe Trp
2676 360          365          370          375
2678 acc gta ccg gct ctc ttc gat aac gtaaaatact atccatctat ttgctatatt      3746
2679 Thr Val Pro Ala Leu Phe Asp Asn
2680          380
2682 cgaagctctt cttgcaagt aaacgcactt aacatataaa tcatctttgt ttaaaccag      3805
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2685 Phe Leu Ala Tyr Phe Tyr Val Ile Phe Leu Thr Leu Leu Leu Phe Asp
2686 385          390          395
2688 tga gccaaagag acgatgaccg atgccgatca aagtaagcac caaatctaaa      3906
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2694 gtttttgtaa aaaggtatgg gaaatattgg aagctgtatt gtgagaaagt caaatacagg      4026
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VERIFICATION SUMMARY

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Input Set : A:\seqlist.txt

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L:259 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19

L:278 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20

L:2690 M:254 E: No. of Bases conflict, LENGTH:Input:400 Counted:3906 SEQ:36